The evolution of the *DGAT2* / *MGAT* gene family

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We investigate the evolution of the *DGAT2* / *MGAT* gene family, which is composed of at least eight members in mammals and has homologues in other vertebrates, invertebrates, and fungi. All members of the family are known or suspected to possess mono- or diacylglycerol acyltransferase activity and to play some role in dietary fat uptake, lipid synthesis, and triglyceride storage. Using both our own sequence information (for cattle and pigs) and information from various online sources, we assembled complete coding sequences for all members of the gene family (and several invertebrate homologues) for at least one species. All members of the family show a conserved intron-exon structure, with exons 3-8 (numbered relative to *DGAT2*) found universally within the family and showing a high degree of length conservation across species and genes. This indicates that the four *DGAT2*-candidate genes (*DC3*, *4*, *6*, and *7*) are likely to be functional genes rather than pseudogenes. Two major structural differences exist across the family. The first is that *DGAT2* has gained an additional first exon relative to the remaining members in which the first exon is homologous with the latter part of exon 2 of *DGAT2*. The second difference is that exons 3 and 4 lack the intervening intron in some members of the family. Cytogenetically, most of the genes exist as chromosomal tandems within mammals: *DGAT2* / *MGAT2*, *MGAT3* / *DC7*, and *DC3* / *DC4* / *DC6*. Only *MGAT1* lacks a known tandem partner. Using a Bayesian approach, we constructed a phylogenetic tree for the family. Our results show two main lineages, corresponding to members that do (*DGAT2*, *MGAT3*, *DC3*, *DC4*, and *DC6*) and do not (*MGAT1*, *MGAT2*, *DC7*) possess intron 3. However, it could not be determined whether this structural change is due to intron loss or exon splitting. The individual gene trees were largely consistent with the known pattern of species relationships. The only exception was the placement of the rodents within mammals, which remains controversial. The overall evolutionary pattern we observed could result from the two rounds of genome duplication hypothesized to have occurred at the base of the vertebrate radiation (the 2R hypothesis). Although adopting this scenario requires one fewer duplication event than other solutions, it also necessitates a concerted pattern of gene losses that we hold to be unlikely. Our results are equivocal with respect to a second hypothesized genome duplication event in ray-finned fishes. No genes in the pufferfish, *Fugu rubripes*, occur as apparent duplicates (excluding tandems). However, because sequencing of the *Fugu* genome is incomplete, we cannot exclude that the partner genes are present but remain unsequenced.